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Figure 1b

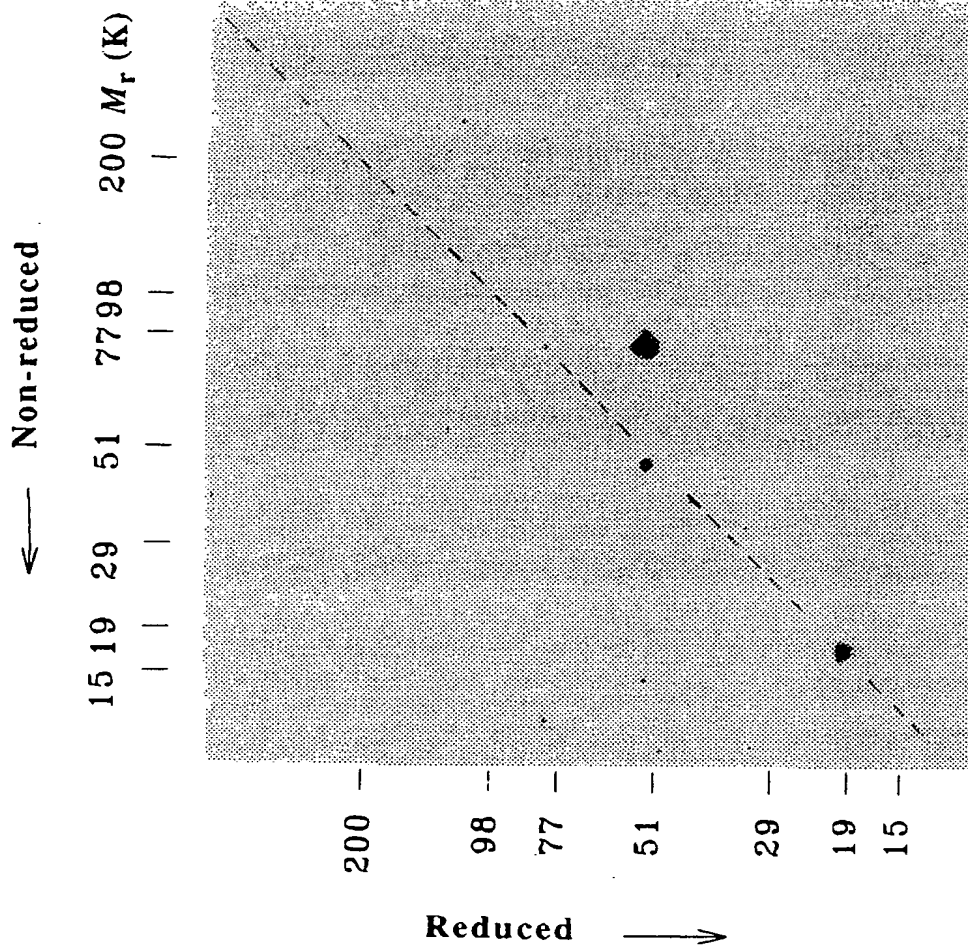
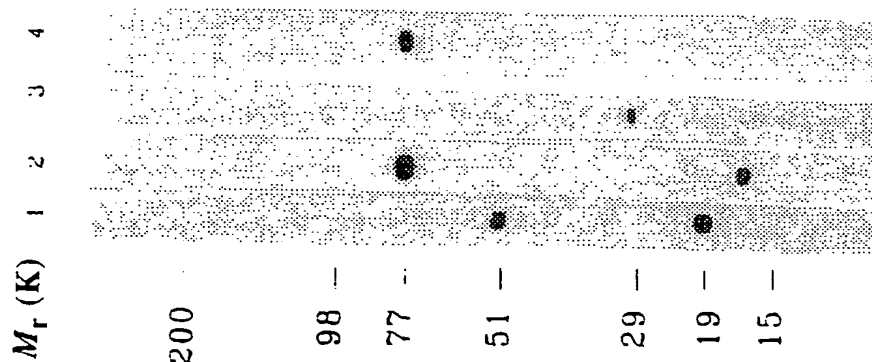


Figure 1a



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Figure 2

MAASP-2	C1r/C1s →		TPLGPKWPEPVFGRRLASPGFPGEYANDQERRWLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLGGQESTDTERAPGKDT	90
MAASP-1			HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGGRETTDTEQTPGQEV	87
C1r			SIPIPKQLFGEVTSPLFPKYPNNFETTTVITVPTGYRVKLVFQQFDLEPSEGGFYDYVKISADKKSRLGRFCGQLGSPLGNPPGKKE	87
C1s			EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLYFTHLDIELSENCAYSVQIISGDTEEGRLCGQRSSNNPHSPIVEE	83
* * * * *				
MAASP-2	EGF →		FYSLGSSLDITFRSDYSNEKP FTGFEAFYAEDIDECO VAPGEA PTCDDHCHNHLGGFYCSERAGYVHLNRKRTCSALCS	170
MAASP-1			VLSPGSFMSITFRSDFSNEER FTGFDHYMAVDVDECK EREDEE LSCDHYCHNYIGGYCSERFGYILHTDNRTORVECS	167
C1r			FMSQGNKMLLTFTDFSNEENGITIMFYKGLLAYQAVALDEASRSKSGEEDPQQOHLCHNYVGGYFCSERPGYELQEDRHSQAQCS	177
C1s			FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINET DFVD VPCSHFONNFIGGYFCSERPPEYFLHDDMKNEGVNCS	161
* * * * *				
MAASP-2	- C1r/C1s →		GOVFTQRSSELSSPEYPRPYKLSCTYSISLEEGFSVILDFV BFPDVFET HPETLCFYPDFLKIQTREEHGPFQKGLTPHR IETKS	256
MAASP-1			DNLFQTQRTGVITSPDFPNPYKSSCELYTIELEEGFMVNLQFE DIFDIED HPEVPCFYPDYIKIKVGPKVLGPFQGEKAPEP ISTQS	253
C1r			SELYTEASGYISSLEYPRSYPPDLRQNSIRVERGLTLHLKFL BFPDIDD HQQVHCFYPDQLQIYANGKNIGEPQKQRPDP LDTSS	263
C1s			GDVFTALIGEIASPNYPKPYPENSRCQYQIRLEKGFQVVTLRREDPVEAADSAGNCLDSLFFVAGDRQFGPYCGHGFPGPLNIETKS	250
* * * * *				
MAASP-2	CCP-1 →		NTVTITFVTDES DHTGWKIHSTTAQPCPYPMAPPN GHVSPVQAKYILKDSFSIFCETGYELLQGHLPKLSFTAVCQKDGSWDRMPA	345
MAASP-1			HSVLILFHSNDSNGENRGWRLSYRAAGNECPQLQPPVH GKIEPSQAKYFFKDQVLVSCTDGYKVLKDNVEMDTFQIECLKDGTSWNKIPT	342
C1r			NAVDLLFPTDES DSGSRGWKLYRTTEIKQPKQKTLDEFTIIQNLPQYQFRDYFIATCKQGYQLIEGNQVLHSFTAVCQDDGTWHRAMP	353
C1s			NALDIIFQTLDTGQKKGWKLRYHGDPMPCPKEDTPN SVNEPAKAKYVFRDVVQITCLDGFVVEGRVGATSFYSTCQSNKGWSNSKLK	338
* * * * *				
MAASP-2	CCP-2 →		CSIVDCGPPDDLPSGRVEYITGPGVTYTKAVIQYSCEETFYTM KVNKGKYVCEADGFWTSSKGEKSLPVEPVGGLS ARTT	426
MAASP-1			CKIVDCRAPGELEHGLITFSTRNLTYYKSEIKYSCEPEYKML NNNTGIYTCQAQGVVMNKVLGRSLPTCLPVGGLPKFSRKL	426
C1r			CKIKDCQPRNLNGDFRYTTTGMVNTYKARIQYQYCEPYKMQTRAGSRESEQGVYTCQAQGIWNEQKGEKIPRELPGVGKPVNPFVEQ	443
C1s			CPVDCGIPESIEENGKVE DPESTLPGSVIRYTCPEPYMYE NGGGGEYHCAGNGSWNEVLGPPELPKCPVPGVPREPFEE	419
* * * * *				
MAASP-2	serine protease →		GGRIYGGQKAKPGDFPWQVLILGGTTA AGALLYDNVWLTAAH AVYEQKHDAASALDIRMGLTKRLSPHYTQAWSEAVFIHEG	507
MAASP-1			MARIFNGRPAQKGTTPWIAMLSHLNGQPFCCGSSLGSSWIVTAACHLHQSLLDPKDPTRLRSDLLSPSD FKIIILGKHWRLSDENEQHLG	515
C1r			RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSASLDVFLGHTNVEELMKLGNHP IRRV	523
C1s			KQRIIGGSDADIKNFPWQVFPDNPWA GGALINEYVWLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG	498
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MAASP-2	YTHDAG		FDNDIALIKLNKVVINSNITPICLPRKEAESFMRTDDIGTAGSWGLTQRGFLARNLMYVDIPIVDHQCTAAYEK	589
MAASP-1			VKHTTLHPKYDPNTFENDVALVELLESFVLNAFVMPICLP EGPQEGAMVIVSGWGKQFLQRPETLMEIEIPIVDHSTQKAY	599
C1r			SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVANPQACEN WLR	608
C1s			WKLELV PEGRTN FDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVE	586
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MAASP-2	PPYPRG		SVTANMLCAGLESQKDSQSGSGGALVFLDS ETERWFVGGIVSWGSMNCGEAGQYGVYTKVINIYIPWIENIISDF	671
MAASP-1			APLKK KVTRDMICAGEKEGGKDACSGSGGPMVTNLR ERGQWYLVGTVSWG DCGKKDRYGVYSYIHNKDWIQRVTGVRN	680
C1r			GKNRMD VFSQNMFCAGHPSLKQDACQSGSGGVFAVRDP NTDRAWATGIVSWG GCSRG YGFYTKVLNLYVDWIKKEMBEED	688
C1s			KPTADAEAYVFTPMNICAGGEK GMDSCQKDSGGGAFVQDPNDKTKFYAAGLVSWG QCGT YGLYTRVKYNYVDWIMKTMQENSTPRED	673
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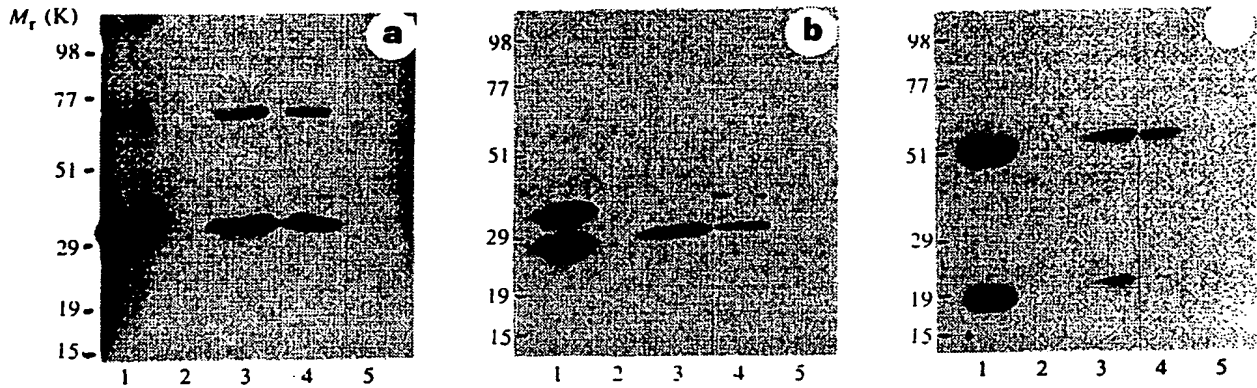
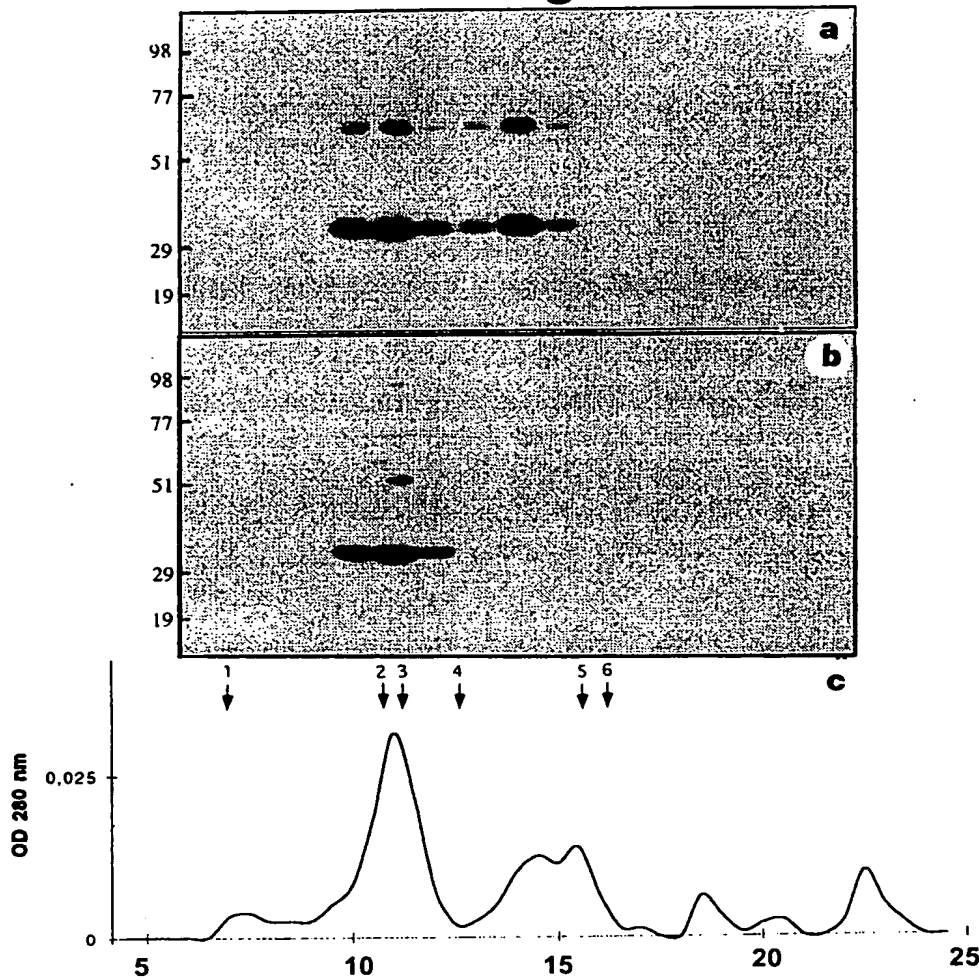


Figure 3b

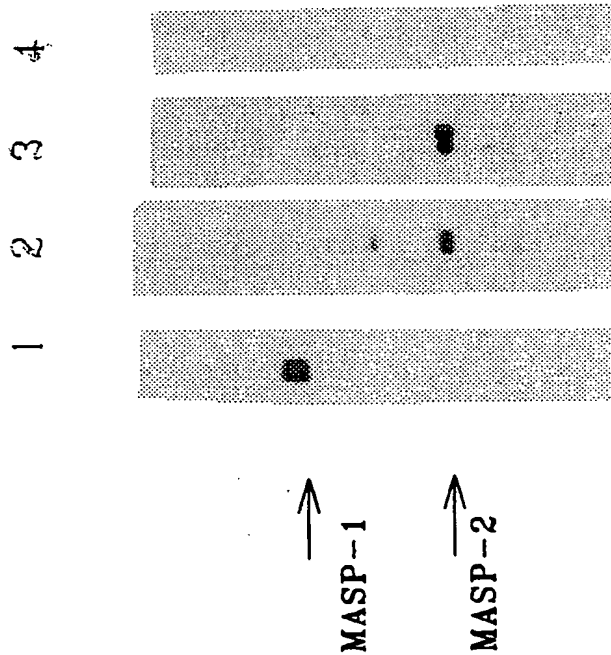


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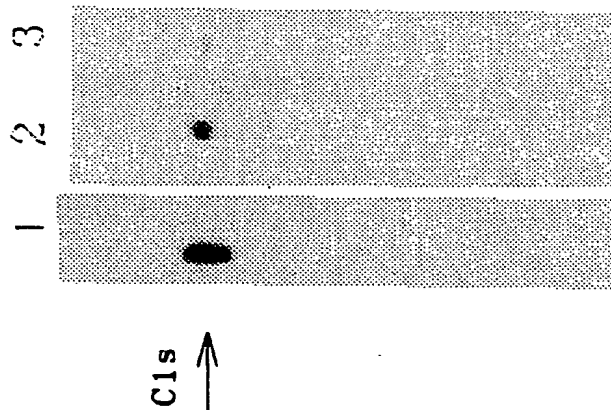
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Figure 4

Blot of MBL preparation

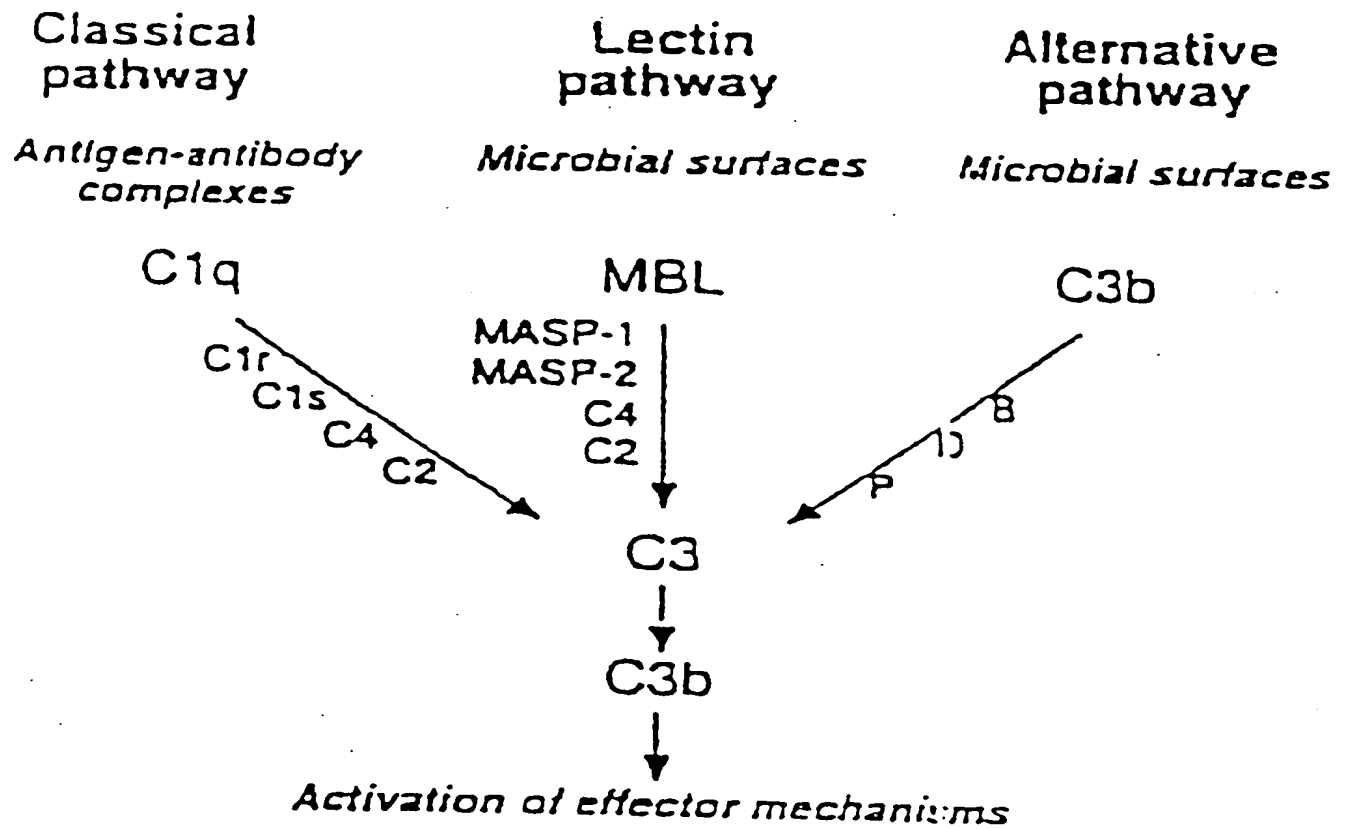


Blot of C1



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Figure 5



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		1
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M R L L T L L G L L C S V A T P L G P K	6	
CGCCTGAACCTGTGTTCCGGCGCCTGGCATCCCCCGGCTTTCAGCGGAGTATGCCAATGACAGGAGCGCGCTCGACCTGACTGCACCCCGGCTA	200	
W P E P V F G R L A S P G F P G E Y A N D Q E R R W T L T A P P G Y	40	
CGCCTGCGCTCTACTTCAACCACTTGGACCTGGAGCTCTCCACCTCTCGGAGTACGACTTCGTCAAGCTGAGCTCGGGGCCAAGCTGCTGGCCAG	300	
R L R L Y F T H F D L E L S H L C E Y D F V K L S S G A K V L A T	73	
CTGTGCGGAGGAGACAGACAGGAGCGGGCCCTTGGCAAGCACTTTCTACTCGCTGGGCTCGGCTGCACATTAACCTTCCGCTCCGACTACT	400	
L C C G Q E S T D T E R A P G K A C T T F Y S L G S S L D I T F R S D Y	106	
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S N E K P P T G F E A F Y A A E D I D E C Q V I P G E A P T C D H H	140	
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C H N H L G O F Y C S C R A G Y V L H R N K R T C S A L C S G Q V	173	
TTCAACCAAGGCTCTGGGAGCTCAGCAGCCCTGAATACCACCGCGGATCCCAACTCTCCAGTTGCATCTACAGCATCAGCCTGCGAGGGGCTCA	700	
F T Q R S G E L S S P E Y P R P Y P K L S S C T Y S I S L E E G F	206	
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R P M P A C S I O V D C G P P D D L P S G R V E Y I T G G P G V T T Y	373	
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G T T H N C G E A G Q Y G V Y T K V I N Y I P A I E N I I S D F stop	671	
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